**Figure 1. Multi-omic Analysis of Enterococcal Bacteremia Patient Plasma.**

1. Workflow for Enterococcal Bacteremia plasma analysis.
2. Distribution of values collected from selected clinical metadata fields across Enterococcal Bacteremia patients.
3. Unsupervised hierarchical clustering of proteomics data as visualized after calculating Euclidian distance and utilizing the Ward.D2 agglomeration method. Colors of branches indicate the species of infection (yellow = healthy volunteer, navy = *E. faecalis*, teal *= E. faecium*) and color of sample id labels represent mortality or survival (black = survival, red = mortality)
4. Unsupervised hierarchical clustering of metabolomic data as visualized after calculating Euclidian distance and utilizing the Ward.D2 agglomeration method. Colors of branches indicate the species of infection (yellow = healthy volunteer, navy = *E. faecalis*, teal = *E. faecium*) and color of sample id labels represent mortality or survival (black = survival, red = mortality)

**Figure 2. Untargeted Proteomics Reveal Dramatic Differences Between Bacteremia Types and Healthy Plasma**

1. Volcano plot comparing log2 fold change and FDR adjusted p values of protein abundances observed when comparing infected to healthy.
2. Significantly enriched GO terms from plasma proteomics of patients suffering from Enterococcal, *E. faecalis*, *E. faecium*, and *S. aureus* bacteremia.
3. Top 2 performing protein biomarkers as ranked using ensemble feature selection. Violin plot statistics indicate results of t tests.
4. Venn diagram displaying the numbers of significantly different proteins (FDR adjusted p value <= 0.05) shared between Enterococcal, *E. faecalis*, *E. faecium*, and *S. aureus* bacteremia when compared to healthy.

**Figure 3. Untargeted Metabolomics Reveal Dramatic Differences Between Enterococcal Bacteremia and Healthy Plasma**

1. Volcano plot comparing log2 fold change and FDR adjusted p values resulting from t tests of normalized metabolite abundances comparing infected to healthy.
2. Count of the number of metabolite features identified in this study.
3. Enrichment analysis of metabolite spectral matches found to be significantly different (p adj <= 0.05) in infected patients relative to healthy. Colors show bile acid class (blue = primary bile aid, teal = conjugated primary bile acid, and green = conjugated secondary bile acid). RID12051 and RID17592 are features corresponding to spectral matches to (((3a,6b,7b)-3,6,7-trihydroxy-24-oxocholan-24-yl)amino)ethanesulfonic acid and (((3a,12b)-3,12-dihydroxy-24-oxocholan-24-yl)amino)ethanesulfonic acid respectively.
4. Evaluation of the top 2 performing metabolite spectral matches as ranked using ensemble feature selection for distinguishing enterococcal bacteremia patients from healthy. Violin plot statistics indicate results of t-tests.

**Figure 4. Untargeted Proteomics Reveals Differences Between *Enterococcus faecalis* and *Enterococcus faecium* Bacteremia.**

1. Volcano plot comparing log2 fold change and FDR adjusted p values of protein abundances observed when comparing *E. faecalis* and *E. faecium* infected patients.
2. GO Term enrichment analysis of the proteins found to be significantly enriched (FDR adjusted p value <= 0.05) in proteins significantly more abundant in Enterococcus faecalis patients relative to Enterococcus faecium.
3. Immunoglobulin abundances compared across patients with *E. faecalis* or *E. faecium* bacteremia and healthy volunteers. Statistics indicate result of t-tests adjusted for multiple comparisons.
4. GO Term enrichment analysis of the proteins found to be significantly enriched in proteins significantly more abundant in Enterococcus faecium patients relative to Enterococcus faecalis.
5. Top 2 performing protein biomarkers as ranked using ensemble feature selection for distinguishing patients infected with *Enterococcus faecalis* from those infected with *Enterococcus faecium*. Violin plot statistics indicate results of t-tests.

**Figure 5. Untargeted Metabolomics Reveals Differences Between *Enterococcus faecalis* and *Enterococcus faecium* Bacteremia.**

1. Volcano plot comparing log2 fold change and FDR adjusted p values resulting from t tests of normalized metabolite abundances comparing *E. faecalis* to *E. faecium*.
2. Evaluation of top 2 performing putatively identified metabolite spectra matches as ranked using ensemble feature selection for distinguishing enterococcal bacteremia patients from healthy. Violin plot statistics indicate results of t-tests.

**Figure 6. Multi-omic Discrimination of Mortality from Survival.**

1. Volcano plot comparing log2 fold change and FDR adjusted p values of protein abundances observed when comparing patients who suffered mortality during admission to those who survived.
2. GO Term enrichment analysis of the proteins found to be significantly enriched (FDR adjusted p value <= 0.05) in mortality relative to survival.
3. GO Term enrichment analysis of the proteins found to be significantly enriched (FDR adjusted p value <= 0.05) in survival relative to mortality.
4. Evaluation of top 2 performing protein biomarkers as ranked using ensemble feature selection for distinguishing mortality from survival. Violin plot statistics indicate results of t tests.
5. Volcano plot comparing log2 fold change and FDR adjusted p values resulting from t tests of normalized metabolite abundances observed when comparing patients who suffered mortality during admission to those who survived.
6. Evaluation of top 2 performing metabolite spectral matches as ranked using ensemble feature selection for distinguishing mortality from survival. Violin plot statistics indicate results of t-tests.